Application No. 10/672,937
Amendment and Reply Dated January 10, 2008
In Response to Office Action Dated October 19, 2007

Amendments to the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of claims:

1.   (Currently amended) ~~An automated~~ A method for ~~sequence evaluation used to compare~~ outputting variants between sample sequence information relating to at least one sample ~~against~~ and reference sequence information relating to at least one reference, the method comprising:

acquiring sample sequence information relating to the at least one sample ~~and to the at least one reference~~;

assembling consensus sequence information from the sample sequence information;

generating rule-based criteria, the rule-based criteria comprising pre-selected rules for at least one of scan position differences, peak height ratios, peak area ratios, and base composition;

~~evaluating the sequence information relating to the at least one sample to identify~~ identifying ambiguous bases present within the ~~sample~~ consensus sequence information by ~~applying a~~ comparing the consensus sequence information to the rule-based criteria, wherein ambiguous bases ~~are distinguished from unambiguous bases on the basis of~~ that do not meet the pre-selected rules for at least one of the ~~following~~ rule-based criteria~~: (a) scan position differences, (b) peak height ratios, (c) peak area ratios, and (d) base composition~~ are labeled ambiguous;

determining what percentage of the bases present within the consensus sequence information are ambiguous bases;

Page 2 of 11

Application No. 10/672,937
Amendment and Reply Dated January 10, 2008
In Response to Office Action Dated October 19, 2007

trimming the consensus sequence information until the percentage of ambiguous bases is

below a user-defined threshold, to form trimmed consensus sequence information;

evaluating the quality and coverage of the sample sequence information in comparison to

the reference sequence information to identify reportable ranges and sequence variants for the

sample sequence information based on a quality value determined at least by the identified

ambiguous bases and unambiguous bases, wherein the reportable ranges comprise base sequence

ranges related to the at least one sample having an associated quality value exceeding a confidence

threshold, and being usable for comparison matching; and

determining variant information between the trimmed consensus sequence information and

the reference sequence information; and

outputting at least the reportable ranges and sequence variants the variant information to a

file user.

2.   (Currently amended) The method of claim 1, wherein the generated rule-based criteria for

assessing comprises pre-selected rules for scan position differences to differentiate between

ambiguous and unambiguous bases further and the method further comprises identifying

differences between scan positions of major and minor peaks, within the sample sequence

information, which fall below an empirical threshold.

Application No. 10/672,937
Amendment and Reply Dated January 10, 2008
In Response to Office Action Dated October 19, 2007

3.   (Original) The method of claim 2, wherein the empirical threshold associated with

identifying differences between scan positions is in the range of approximately 0 to approximately

3.

4.   (Currently amended) The method of claim 1, wherein the generated rule-based criteria for

assessing comprises pre-selected rules for scan position differences for differentiating between

ambiguous and unambiguous bases further and the method further comprises identifying

differences between scan positions of major and minor peaks within the sample sequence

information, which reside above, below, or are substantially equivalent to, a user-defined threshold.

5.   (Currently amended) The method of claim 1, wherein the generated rule-based criteria for

assessing comprises pre-selected rules for peak height ratios to differentiate between ambiguous

and unambiguous bases further and the method further comprises assessing identifying differences

between peak height ratios for major and minor peaks, within the sample sequence information,

which exceed an empirical threshold.

6.   (Currently Amended) The method of claim 5, wherein the empirical threshold associated

with assessing the peak height ratios is in the range of approximately 0.3 to approximately 1.0.

7.   (Currently amended) The method of claim 1, wherein the generated rule-based criteria for

assessing comprises pre-selected rules for peak height area ratios for differentiating between

Page 4 of 11

Application No. 10/672,937
Amendment and Reply Dated January 10, 2008
In Response to Office Action Dated October 19, 2007

~~ambiguous and unambiguous bases further~~ and the method further comprises ~~assessing~~ identifying differences between peak area ratios of major and minor peaks, within the sample sequence information, which reside above, below, or are substantially equivalent to, a user-defined threshold.

8.   (Currently amended) The method of claim 1, wherein the generated rule-based criteria ~~for assessing~~ comprises pre-selected rules for peak area ratios ~~to differentiate between ambiguous and unambiguous bases further~~ and the method further comprises ~~assessing~~ identifying differences between peak area ratios for major and minor peaks, within the sample sequence information, which exceed an empirical threshold.

9.   (Currently amended) The method of claim 8, wherein the empirical threshold associated with ~~assessing~~ the peak area ratios is in the range of approximately 0.3 to approximately 1.0.

10.   (Currently amended) The method of claim 1, wherein the generated rule-based criteria ~~for assessing~~ comprises pre-selected rules for peak area ratios ~~for differentiating between ambiguous and unambiguous bases further~~ and the method further comprises ~~assessing~~ identifying differences between peak area ratios of major and minor peaks, within the sample sequence information, which reside above, below, or are substantially equivalent to, a user-defined threshold.

11.   (Currently amended) The method of claim 1, wherein the generated rule-based criteria ~~for assessing~~ comprises pre-selected rules for base composition ~~to differentiate between ambiguous and~~

Application No. 10/672,937
Amendment and Reply Dated January 10, 2008
In Response to Office Action Dated October 19, 2007

~~unambiguous bases further~~ and the method further comprises <u>determining major and minor peaks</u>

<u>within the sample sequence information and</u> determining if the major and minor peaks within the

sample sequence information are both purines or both pyrimidines.

12.   (Canceled).

13.   (Currently amended) The method of claim 1, wherein the <u>generated</u> rule-based criteria ~~for~~

~~distinguishing between ambiguous and unambiguous bases~~ comprises <u>pre-selected rules for</u>

identifying consecutive runs of bases exceeding an empirical threshold.

14.   (Currently Amended) The method of claim 13, wherein the empirical threshold ~~associated~~

~~with comprises identifying~~ <u>for comparing</u> consecutive runs of bases is in the range of approximately

10 to approximately 13.

15.   (Currently amended) The method of claim 1, wherein the <u>generated</u> rule-based criteria ~~for~~

~~distinguishing between ambiguous and unambiguous bases identifies~~ <u>further comprises identifying</u>

consecutive runs of bases which reside above, below, or are substantially equivalent to a user-

defined threshold.

Page 6 of 11

Application No. 10/672,937
Amendment and Reply Dated January 10, 2008
In Response to Office Action Dated October 19, 2007

16.   (Currently amended) The method of claim 1, ~~wherein~~ further comprising:

excluding identified ambiguous bases ~~are excluded~~ from the ~~evaluation of quality and~~

~~coverage of the~~ sample sequence information and assembling exclusionary consensus sequence

information; and

determining variant information between the exclusionary consensus sequence information

and the reference sequence information.

17.   (Canceled)

18.   (Currently Amended) The method of claim 1, wherein the sample sequence information

relating to the at least one sample and the reference sequence information relating to the at least one

reference ~~comprises~~ comprise mitochondrial DNA sequence information.

19-44. (Canceled)

45.   (New) The method of claim 1, wherein the identifying ambiguous bases further comprises

assigning a quality value to those bases that have been identified as ambiguous.

46.   (New) The method of claim 1, wherein trimming the consensus sequence information

comprises trimming the edges of the consensus sequence information.

Page 7 of 11

Application No. 10/672,937
Amendment and Reply Dated January 10, 2008
In Response to Office Action Dated October 19, 2007

47.   (New) A computer readable medium having stored thereon instructions which cause a

general purpose computer to perform the steps of:

      acquiring sample sequence information relating to the at least one sample;

      assembling consensus sequence information from the sample sequence information;

      generating rule-based criteria, the rule-based criteria comprising pre-selected rules for at

least one of scan position differences, peak height ratios, peak area ratios, and base composition;

      identifying ambiguous bases present within the consensus sequence information by

comparing the consensus sequence information to the rule-based criteria, wherein bases that do not

meet the pre-selected rules for at least one of the rule-based criteria are labeled ambiguous;

      trimming the consensus sequence information until the percentage of ambiguous bases is

below a user-defined threshold, to form trimmed consensus sequence information;

      determining variant information between the trimmed consensus sequence information and

the reference sequence information; and

      outputting the variant information to a user.

Page 8 of 11